

Figure S1.

B.juA005498-B.jPHL2a1	MY-SAIRSLPLDGGDYHGPLDGTNLPGDACLVLTDPKPRLRWTAELHERFVDAVTQLGG	59
B.juB039462-B.jPHL2b1	MYSAAIRSLPLD-GDYHGPLDGTNLPGDACLVLTDPKPRLRWTAELHERFVDAVTQLGG	59
B.jMYB1	XXXXXXXXXX	0
B.juA012774-B.jPHL2a	-MYSAIRSLPLDGGEHGPLDGTNLPGDACLVLTDPKPRLRWTAELHERFVEAVTELGG	59
B.juB032221-B.jPHL2b	-MYSAIRSLADGGEHGPLDGTNLPGDACLVLTDPKPRLRWTAELHEKFVEAVTELGG	59
B.juA005498-B.jPHL2a1	PDKATPKTIMRTMGVKGLTLYHLKSHLQKFRLGRQACKDSTDNS-KDASCVGESQDTGSS	118
B.juB039462-B.jPHL2b1	PEKATPKTIMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTENS -KDASCVGESQDTGSS	118
B.jMYB1	----- MGVKGLTLHYHLKSHLQKFRLGRQACKESTENS-KDASCVGESQDTGSS	47
B.juA012774-B.jPHL2a	PEKATPKTLMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTDNSNKDASCVGESQDTGSS	119
B.juB032221-B.jPHL2b	PEKATPKTLMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTDNS-KDASCVGESQDTGSS	118
*****:*****:*****:*****:*****:*****:*****:*****:*****:*****		
B.juA005498-B.jPHL2a1	SSSSLRMAAQEQNEGQVTEALRAQMEVQRRLHEQLEHGQVQRRQLQLRIEAQGKYLQSIL	178
B.juB039462-B.jPHL2b1	SSSSLRMAAQEQNEGQVTEALRAQMEVQRRLHEQLE --- VQRRQLQLRIEAQGKYLQSIL	175
B.jMYB1	SSSSLRMAAQEQNEGQVTEALRAQMEVQRRLHEQLEYQQVQRRQLQLRIEAQGKYLQSIL	107
B.juA012774-B.jPHL2a	SPSSLKLAAQEQNESYQVTEALRAQMEVQRRLHEQLE---VQRRLQVRIEAQGKYLQSIL	176
B.juB032221-B.jPHL2b	SPSSLRLAAQEQQNEGQVTEALRAQMEVQRRLHEQLE---VQRRLQVRIEAQGKYLQSIL	175
* ***:*****:*****:*****:*****:*****:*****:*****:*****		
B.juA005498-B.jPHL2a1	EKACKAFDDQAAFGLEAAREELSELATIKVSNSSQGT-AVPFFDTKM-MMMPSLSELA	236
B.juB039462-B.jPHL2b1	EKACQAFDDQAAFGLEAAREELSELATIKVS---QGT-AVPFLDATKM-MMMPSLSELE	230
B.jMYB1	EKACQAFDDQAAFGLEAAREELSELATIKVS---QGT-AVPFLDATKM-MMMPSLSELE	162
B.juA012774-B.jPHL2a	EKACKAFDEQAAMFTGLEAREELSELATIKVSNSSQGA-TVPYFDATKMMMPMSLSELE	235
B.juB032221-B.jPHL2b	EKACKAFEEQAVTFGGLETAREEELSDLATIKASSSSQTTTVPYFDATKMMMPMSLSELE	235
*****:*****:*****:*****:*****:*****:*****:*****:*****		
B.juA005498-B.jPHL2a1	VAV-DTK-NNITTNCSESSLTSNTNGSSVAAASMKKRLRGDDVGLGYEAGWNVPSSTI	294
B.juB039462-B.jPHL2b1	VAI-DTK-NNITTNCSESSLTSNTNGSSVAAASMKKRHRGDDVGLGYEAGWIVPSSTIG	288
B.jMYB1	VAI-DTK-NNITTNCSESSLTSNTNGSSVAAASMKKRHRGDDVGLGYEAGWIVPSSTIG	220
B.juA012774-B.jPHL2a	VAAIDHKSNIITTCSESSLTSNTNGSSVAAASMKKRHRGGD-NVGYEGSWTVPGSTMG	294
B.juB032221-B.jPHL2b	VAAIDQKSNIT-TNCSESSLTSNTNGSSVAAASMKKRHRG-D-SVGYEASWIMPSSTIG	292
** * * * *****:*****:*****:*****:*****:*****:*****		
B.juA005498-B.jPHL2a1	G	295
B.juB039462-B.jPHL2b1	-	288
B.jMYB1	-	220
B.juA012774-B.jPHL2a	-	294
B.juB032221-B.jPHL2b	-	292

Figure S1. Multiple sequence alignment of BjPHL2 subclade members.

The protein sequences of all BjPHL2 subclade members are aligned with

Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The 71-amino acid-long deletion at the N-terminal and a YGQ insertion in the central between BjMYB1 and BjPHL2b1 are indicated in yellow box.

Figure S2.

B.jMYB1

B.juB039462-B.jPHL2b1

0

ATGTAECTCGCGCGATTGGCTGCTTCCTCTGACGGTACTACCAGGACCTTTGAC 60

B.jMYB1

B.juB039462-B.jPHL2b1

0

GGTACTAATCTCCCGGCACGCCGTGGCTTAACCACTGACCCAAACCCGTCTT 120

B.jMYB1

B.juB039462-B.jPHL2b1

0

CGGTGGACCGCGGAGCTCACGAGAGGTTGACGCCGTACCGCAGCTGGTCCC 180

B.jMYB1

B.juB039462-B.jPHL2b1

ATGGGAGTGAAAGGCCTCACCCCTAC 27

GAAAAACGACGCCAAACTATCATGAGAACAAATGGGAGTGAAAGGCCTCACCCCTAC 240

B.jMYB1

B.juB039462-B.jPHL2b1

CACCTCAAATCACATCTCCAGAAATTCCGGCTAGGGAGGCAAGCTTGTAAAGAATCACT 87

CACCTCAAATCACATCTCCAGAAATTCCGGCTAGGGAGGCAAGCTTGTAAAGAATCACT 300

B.jMYB1

B.juB039462-B.jPHL2b1

GAGAACTCCAAGGATGCTCTTGTGTTGGGAGAGTCAGGACACAGGTTATTCATCG 147

GAGAACTCCAAGGATGCTCTTGTGTTGGGAGAGTCAGGACACAGGTTATTCATCG 360

B.jMYB1

B.juB039462-B.jPHL2b1

TCATCACTGAGAATGGCAGCGCAGGAGCAGAACGAGGGTACCAAGTCAGTCAAGCTCTA 207

TCATCACTGAGAATGGCAGCGCAGGAGCAGAACGAGGGTACCAAGTCAGTCAAGCTCTA 420

B.jMYB1

B.juB039462-B.jPHL2b1

CGCGCTCAAATGGAAGTCAAAGAAGACTACAGGACAATTGGAGTATGGGAGGTACAA 267

CGCGCTCAAATGGAAGTCAAAGAAGACTACAGGACAATTGGAGGTACAA 471

B.jMYB1

B.juB039462-B.jPHL2b1

CGGAGACTCCAGCTGAGGATAGAGGCACAAGGAAAGTACTTACAATCGATCCTTGAGAAA 327

CGGAGACTCCAGCTGAGGATAGAGGCACAAGGAAAGTACTTACAATCGATCCTTGAGAAA 531

B.jMYB1

B.juB039462-B.jPHL2b1

GCTTGCCAGGCCTTGACGACCAAGCTGCTGCTTTGTTGGCTCGAGGCAGCTAGGGAA 387

GCTTGCCAGGCCTTGACGACCAAGCTGCTGCTTTGTTGGCTCGAGGCAGCTAGGGAA 591

B.jMYB1

B.juB039462-B.jPHL2b1

GAGCTATCAGAGCTAGCCATCAAAGTGTCTAAGGAACAGCAGTCCGTTAGATGCA 447

GAGCTATCAGAGCTAGCCATCAAAGTGTCTAAGGAACAGCAGTCCGTTAGATGCA 651

BjMYB1	ACAAAGATGATGATGCCATCTTGTCTGAGCTTGAAGTAGC	507
BjuB039462-BjPHL2b1	ACAAAGATGATGATGCCATCTTGTCTGAGCTTGAAGTAGC	711
	*****	*****
BjMYB1	AACATCACACCAACTGTCGTTGAAAGCTCTGACTTCAACACCAATGGGAGCTG	567
BjuB039462-BjPHL2b1	AACATCACACCAACTGTCGTTGAAAGCTCTGACTTCAACACCAATGGGAGCTG	771
	*****	*****
BjMYB1	GTTTCTGCTGCATCGATGAAGAAGCGGCATCGTGAGACGATGTAGGCCTAGGGTACGAG	627
BjuB039462-BjPHL2b1	GTTTCTGCTGCATCGATGAAGAAGCGGCATCGTGAGACGATGTAGGCCTAGGGTACGAG	831
	*****	*****
BjMYB1	GCAGGGTGGATTGTGCCTAGTAGTACCATGGATAA	663
BjuB039462-BjPHL2b1	GCAGGGTGGATTGTGCCTAGTAGTACCATGGA---	864
	*****	*****

Figure S2. Sequence alignment of BjMYB1 and BjPHL2b1 at the CDS

level. The CDS sequences of BjMYB1 and BjPHL2b1 are aligned with Clustal Omega. The observed 213 nt absence in the 5' end, 9 nt insertion in the central and a G to A replacement at 3' end between BjMYB1 and BjPHL2b1 are indicated by yellow box.

Figure S3.

B.juB039462-BjPHL2b1	MYSAAIRSLPLGDYHGPLDGTNLPGDACLVTTDPKPRLRWTAEHLHERFVDAVTQLGGP	60
B.jMYB1	-----	0

B.juB039462-BjPHL2b1	EKATPKTIMRTMGVKGLTLYHLKSHLQKFRLGRQACKESTENSKDASCVGESQDTGSSSS	120
B.jMYB1	-----MGVKGLTLYHLKSHLQKFRLGRQACKESTENSKDASCVGESQDTGSSSS	49

B.juB039462-BjPHL2b1	SSLRMAAQEQNEGYYQVTEALRAQMEVQRRLHEQLE	177
B.jMYB1	SSLRMAAQEQNEGYYQVTEALRAQMEVQRRLHEQLEYGQVQRRLQLRIEAQGKYLQSILEK	109

B.juB039462-BjPHL2b1	ACQAFDDQAAAFVGLEAAREELSELAIKVSQGTAVPF DATKMMMPSLSELEVADTKN	237
B.jMYB1	ACQAFDDQAAAFVGLEAAREELSELAIKVSQGTAVPF DATKMMMPSLSELEVADTKN	169

B.juB039462-BjPHL2b1	NITTCNSVESSLTSNTNGSSVSAASMKKRHRGDDVGLGYEAGWIVPSSTIG	288
B.jMYB1	NITTCNSVESSLTSNTNGSSVSAASMKKRHRGDDVGLGYEAGWIVPSSTIG	220

Figure S3. Sequence alignment of BjMYB1 and BjPHL2b1 at the protein level. The protein sequences of BjMYB1 and BjPHL2b1 are aligned with Clustal Omega. The observed 71-amino acid-long deletion at the N-terminal and a YGQ insertion in the central between BjMYB1 and BjPHL2b1 are indicated in yellow box.

Figure S4.

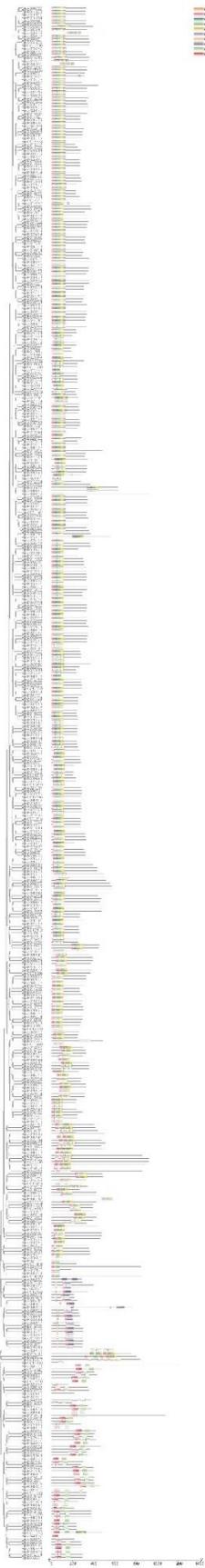


Figure S4. Protein architecture of BjMYBs. The distribution of conserved motifs identified from 502 BjMYB proteins are predicted using the MEME (Multiple Em for Motif Elicitation) tool. Each motif is represented by a number in colored box. See Table S2 for detailed motif information.